Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:32:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238043.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6238043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238043.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:32:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,159,786
Mapped reads	1,845,333 / 85.44%
Unmapped reads	314,453 / 14.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,408 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	171,730 / 7.95%
Duplication rate	7.36%
Clipped reads	882,301 / 40.85%

2.2. ACGT Content

Number/percentage of A's	35,005,624 / 28.67%
Number/percentage of C's	22,714,911 / 18.6%
Number/percentage of T's	38,333,312 / 31.39%
Number/percentage of G's	25,827,038 / 21.15%
Number/percentage of N's	238,250 / 0.2%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0395

Standard Deviation	0.5052

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

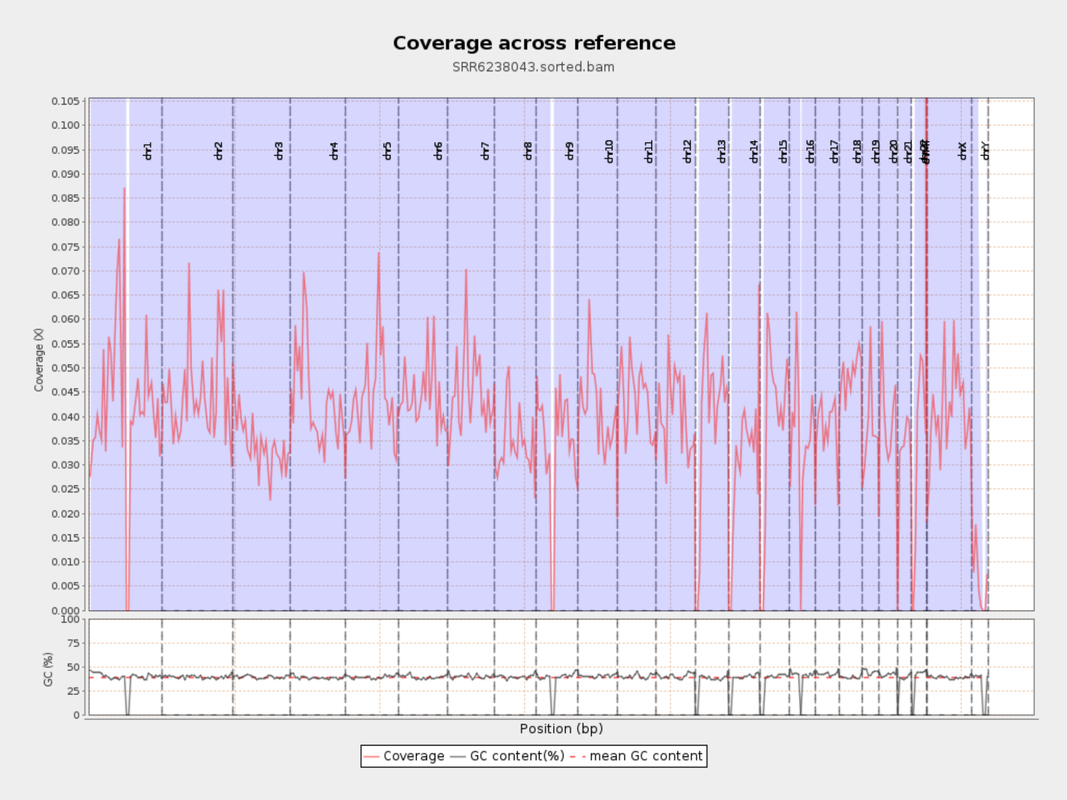
General error rate	0.96%
Mismatches	1,150,536
Insertions	10,584
Mapped reads with at least one insertion	0.57%
Deletions	39,421
Mapped reads with at least one deletion	2.11%
Homopolymer indels	46.75%

2.6. Chromosome stats

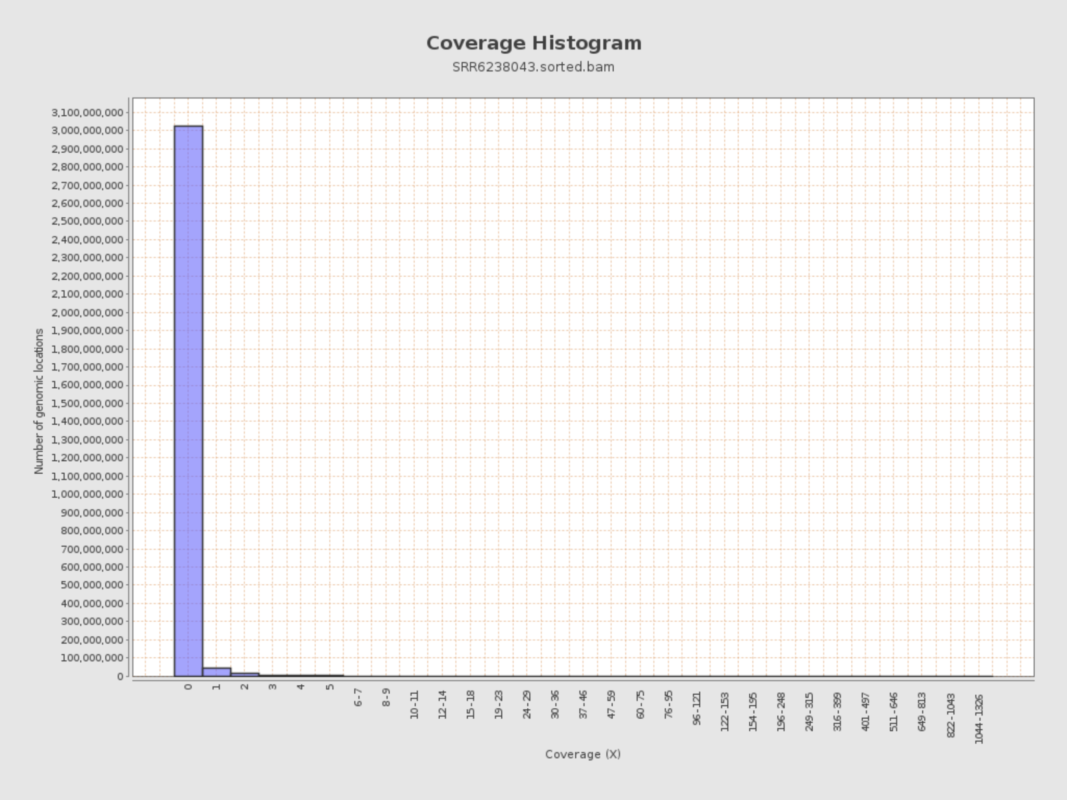
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10662631	0.0428	1.1746
chr2	243199373	10890962	0.0448	0.4877
chr3	198022430	6801743	0.0343	0.2929
chr4	191154276	8318578	0.0435	0.343
chr5	180915260	7902815	0.0437	0.3306
chr6	171115067	7560152	0.0442	0.3536
chr7	159138663	7192467	0.0452	0.5579

chr8	146364022	4986277	0.0341	0.5671
chr9	141213431	4762404	0.0337	0.3721
chr10	135534747	5654589	0.0417	0.399
chr11	135006516	5820973	0.0431	0.3761
chr12	133851895	5421969	0.0405	0.3222
chr13	115169878	4461427	0.0387	0.3136
chr14	107349540	3136376	0.0292	0.2748
chr15	102531392	3945395	0.0385	0.3091
chr16	90354753	3205617	0.0355	0.306
chr17	81195210	3021598	0.0372	0.3191
chr18	78077248	3818893	0.0489	0.6375
chr19	59128983	2197739	0.0372	0.6598
chr20	63025520	2547130	0.0404	0.3252
chr21	48129895	1533548	0.0319	0.2917
chr22	51304566	1614352	0.0315	0.2739
chrMT	16571	37124	2.2403	2.5519
chrX	155270560	6340034	0.0408	0.3362
chrY	59373566	349150	0.0059	0.1416

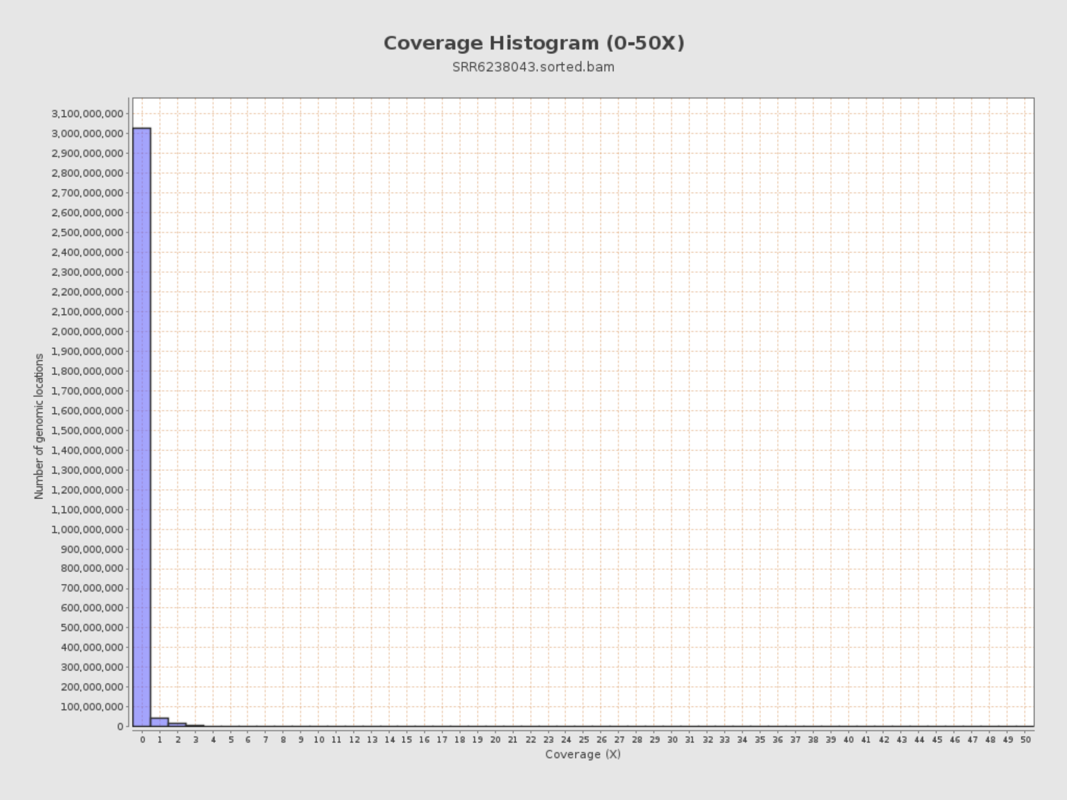
3. Results : Coverage across reference



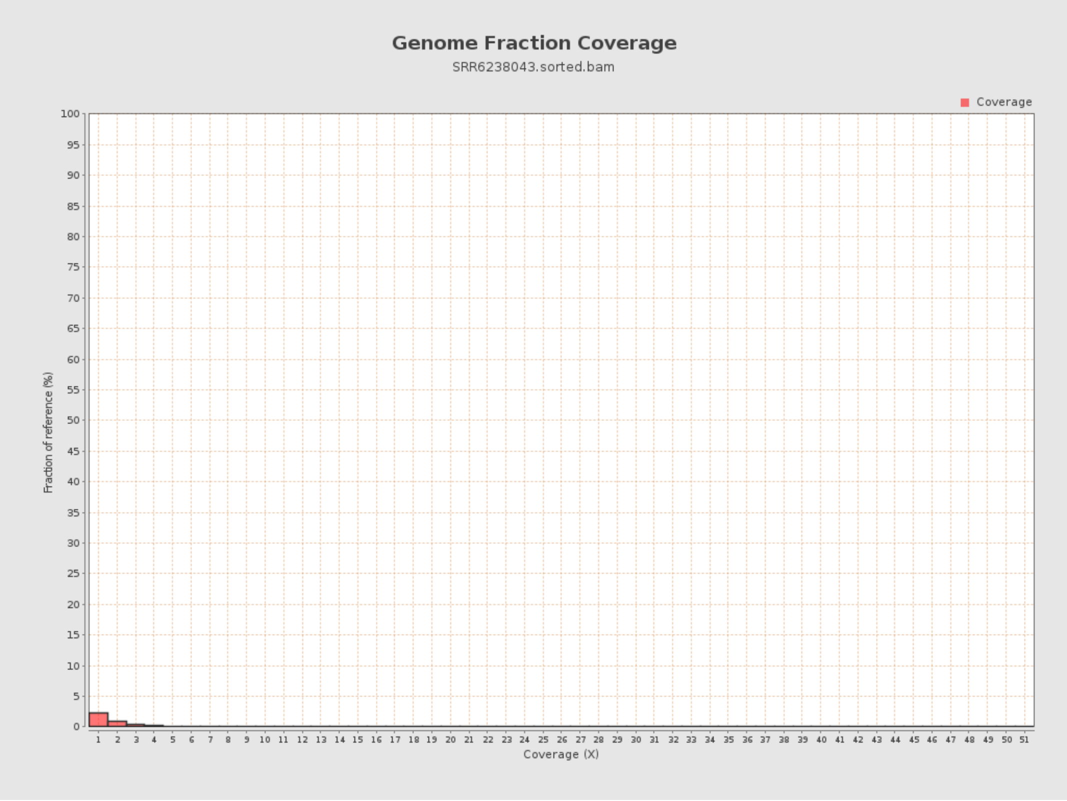
4. Results : Coverage Histogram



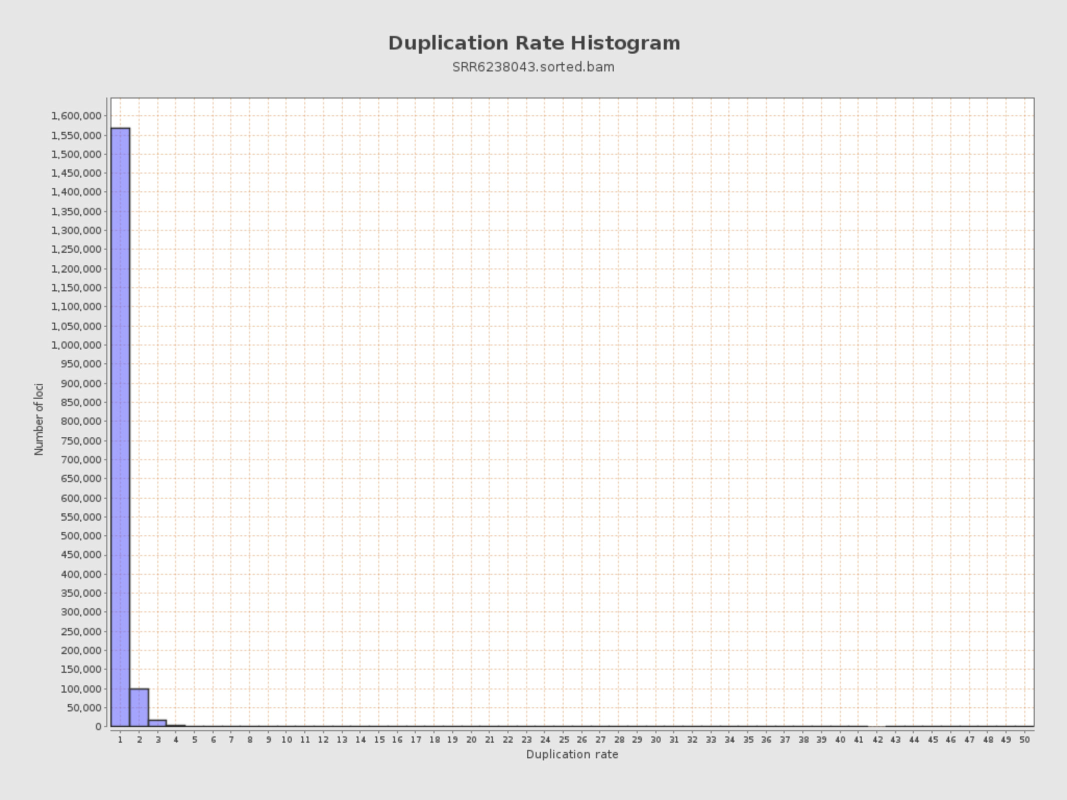
5. Results : Coverage Histogram (0-50X)



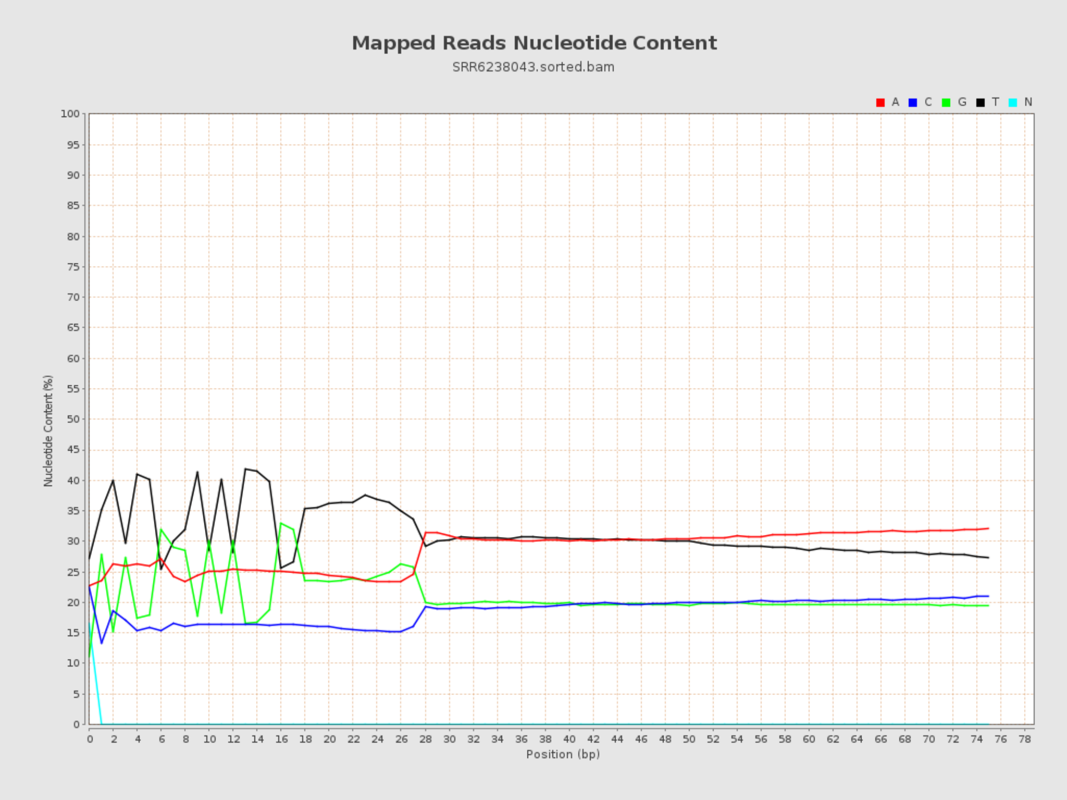
6. Results : Genome Fraction Coverage



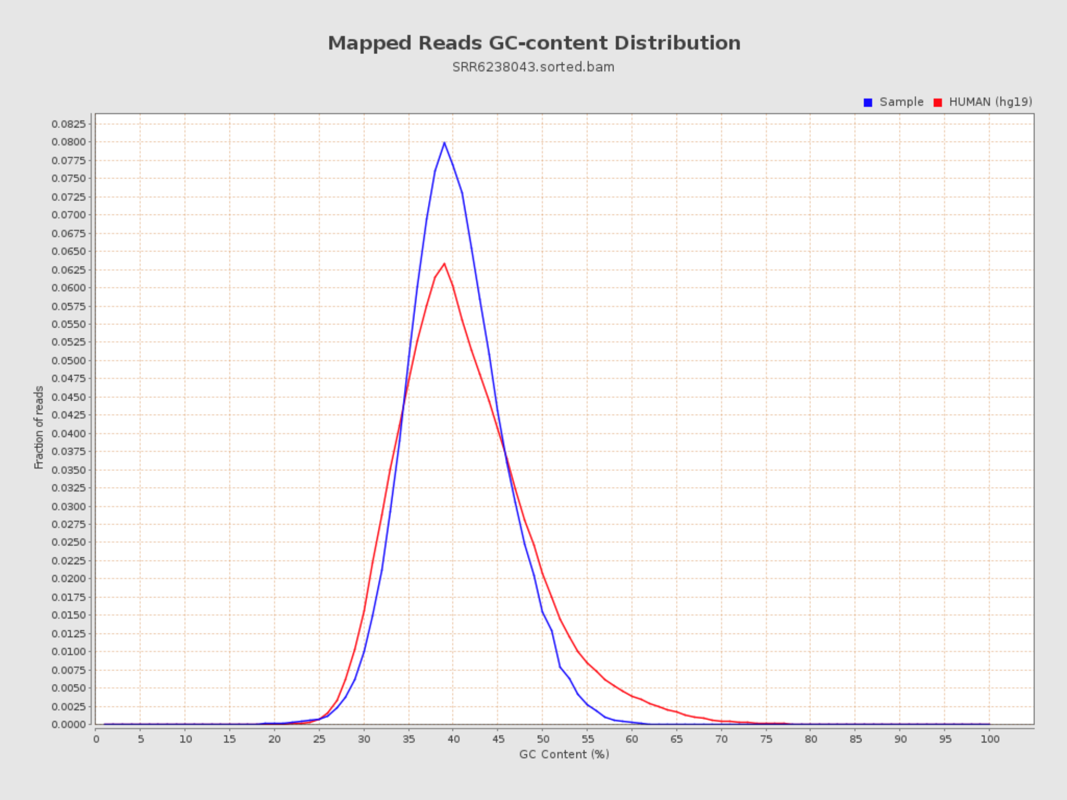
7. Results : Duplication Rate Histogram



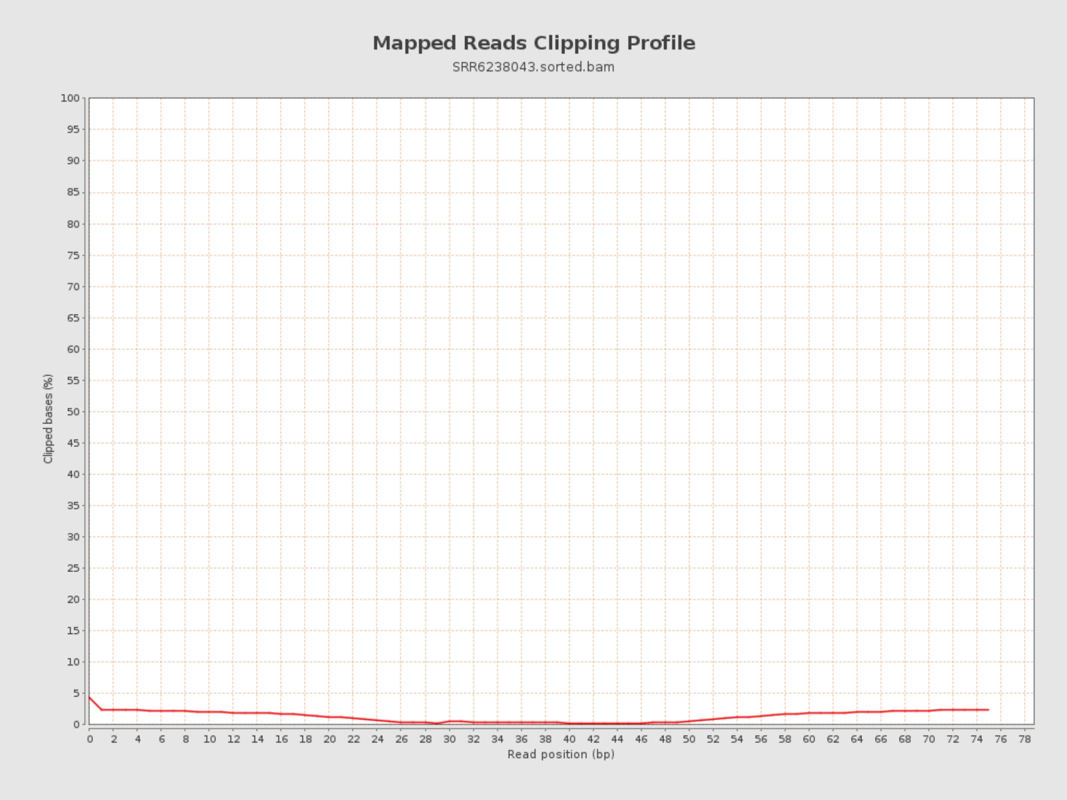
8. Results : Mapped Reads Nucleotide Content



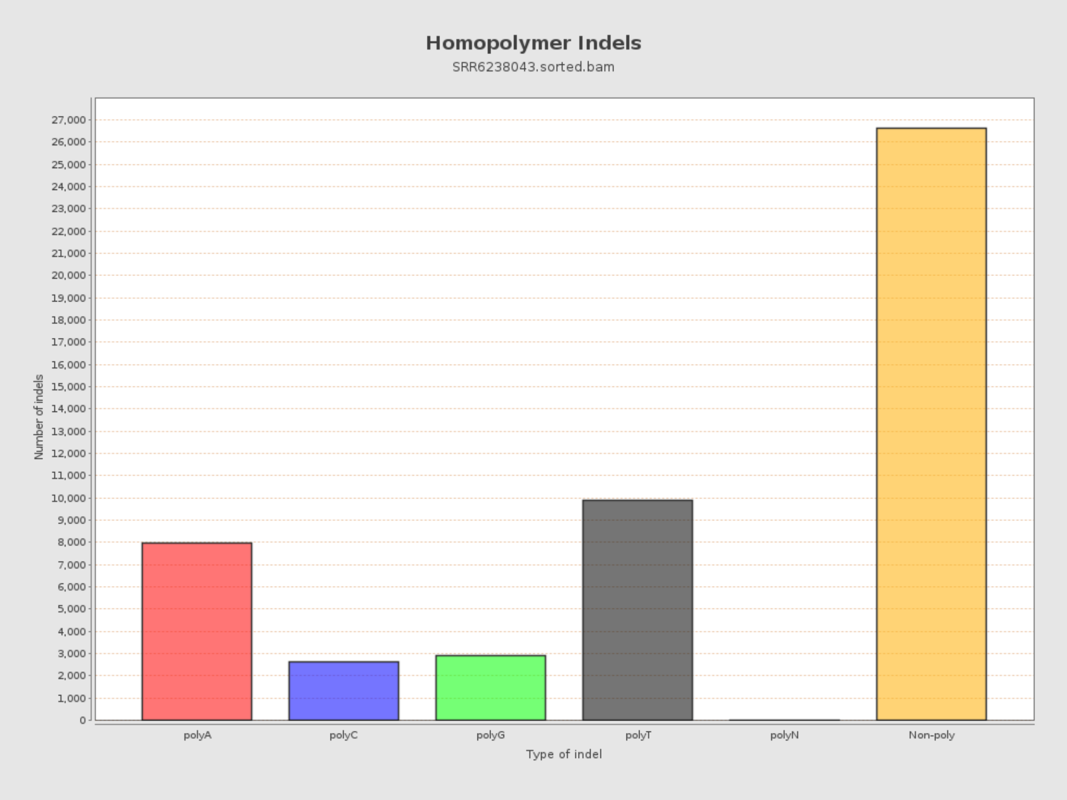
9. Results : Mapped Reads GC-content Distribution



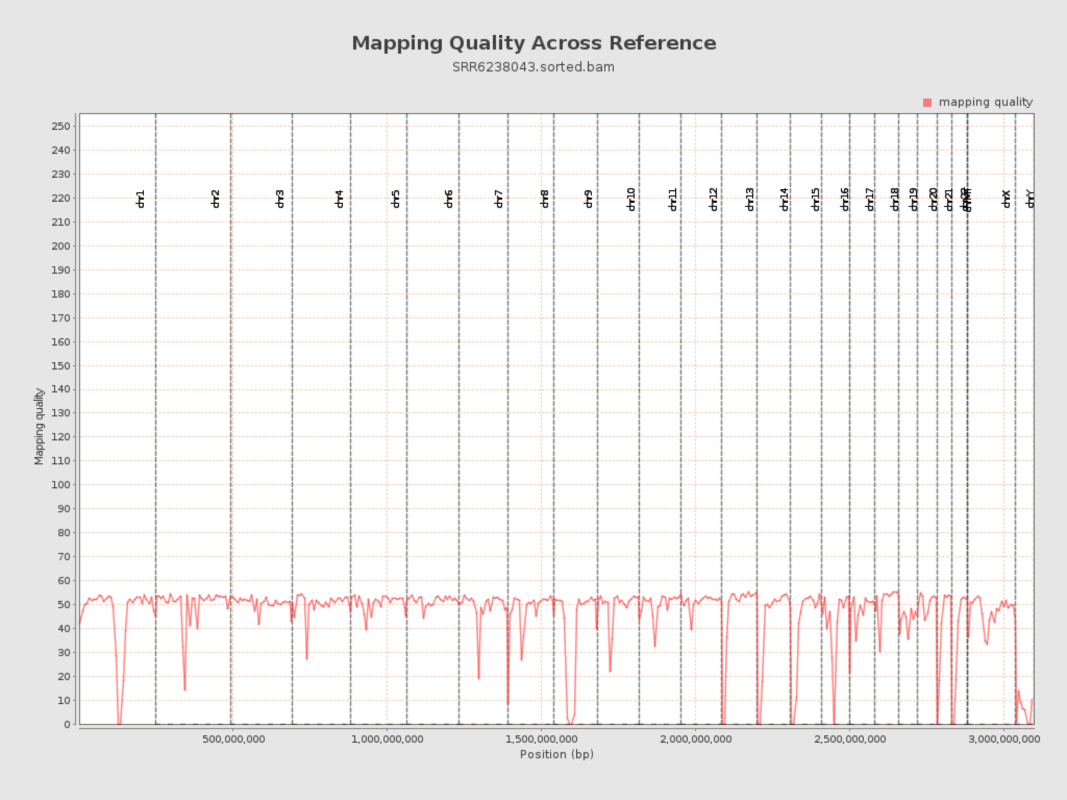
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram